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JOURNAL OF BIOENERGETICS AND BIOMEMBRANES

Volume 28, Number 1 **February 1996**

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Minireview Series: Membrane Protein Crystallization

Guest Editor: Janusz M. Sowadski

Front outside cover: A stereo view of the superimposed images of *E. coli* OmpF porin in two different detergents, as determined by single-crystal neutron diffraction (Pebay-Peyroula *et al.*, 1995). The blue contours are from the detergent ring created by N,N-dimethyldecylamine-*n*-oxide (DDAO) and the green contours are from β-OG. Under the conditions of the experiment, only the hydrophobic core of the detergent rings is well visualized while the detergent head groups are not well resolved. In the upper panel a porin trimer is viewed down its molecular 3-fold axis showing the detergent ring extending out from the protein surface (represented by the violet α-carbon skeleton superimposed on the map). In the lower panel the contact surfaces between two porin trimers in the crystal are shown. While the protein–protein contacts are made, the head groups of the detergents, which are not resolved here, but against each other; it is obvious that changes in the detergent structure could disrupt these contact sites. Photographs are courtesy of Drs. P. Timmins and E. Pebay-Peyroula (ILL, Grenoble).

// JOURNAL OF BIOENERGETICS AND BIOMEMBRANES

Volume 28, Number 2 April 1996

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Minireview Series: Mitochondrial Channels

Series Editor: Carmen Mannella

Front outside cover, Upper: Schematic representation of ion channels that have been identified in mitochondrial membranes. Acronyms and symbols are defined in article by Mannella starting on page 89. *Lower:* Three-dimensional structure of a rat-liver mitochondrion obtained by electron tomography (Mannella *et al.*, 1994, *Microscopy Research and Technique* 27:278–283). Each intracristal compartment is indicated by a different color.

JOURNAL OF BIOENERGETICS AND BIOMEMBRANES

Volume 28, Number 3 **June 1996**

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Minireview Series: Ion Channels in Plasma Membrane Signal Transduction

Series Editor: William A. Catterall

Front outside cover: Subunit structures of ion channels. *Center:* A cross-section and an *en face* view of a phospholipid bilayer membrane containing a hypothetical ion channel consisting of four subunits or domains surrounding a central pore, as in the voltage-gated ion channels. Carbohydrate moieties are illustrated as curving lines. *Top:* The primary structure of the principal subunit of a sodium or calcium channel is illustrated as a transmembrane folding diagram based on analysis of the hydrophobicity of the amino acid sequence. Note the four repeating domains which surround the central pore as illustrated in the drawing in the *center.* Predicted transmembrane alpha helices are illustrated as cylinders. The remainder of the polypeptide chain is illustrated as a bold line with the length of each segment approximately proportional to the length of its amino acid sequence. Red, the S4 segments that serve as voltage sensors; green, the S5, S6, and P segments that line the pore; yellow, the inactivation gate segment that closes over the intracellular mouth of the pore during inactivation. *Left, Right:* The primary structures of a voltage-gated potassium channel and a calcium-activated potassium channel, respectively. Note that each is analogous in structure to one domain of a sodium or calcium channel. Color coding is the same as for the drawing at the *top.*

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JOURNAL OF BIOENERGETICS AND BIOMEMBRANES

Volume 28, Number 4 **August 1996**

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Minireview Series: Gap Junction Membrane Channels

Series Editor: Gina E. Sosinsky

Front outside cover: Schematic illustration of gap junction structure overlaid on a filtered image of frozen-hydrated connexons (see Fig. 1 in the article by Sosinsky for an explanation of the illustration). The original micrograph of a crystalline single connexon layer can be seen in Ghoshroy *et al.* (1995). *J. Membr. Biol.* 146:15–28. The filtered image was obtained computationally by applying both a band pass filter and a periodic mask made with the crystal lattice parameters to its Fourier transform. In this image, protein is displayed black, ice as white, and the membrane between the connexon is displayed as gray. The connexons appear as dark hexagonally-shaped units.

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Volume 28, Number 5 **October 1996**

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Minireview Series: ATP Synthase: Current Views About Subunit Movements During Catalysis

Series Editor: Peter L. Pedersen

Front outside cover: Schematic of the *E. coli* ATP synthase depicting the arrangement of the ε subunit within the stalk region (see Capaldi *et al.,* this issue).

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Volume 28, Number 6 **December 1996**

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Front outside cover: Working model of the Cl^--stimulated, Cl^--translocating ATPase, or Cl^- pump (see Gerencser and Purushotham, this issue).